

```

NGCGGTCAAGCTTGAGGCGTCATCTGGCTGCGCCTAGTGGGCCGTTGCCTTACAGTTGCTGAGAGGAGGTGAGAGGCGG
                                     M K
GGGCGCTAGGGCCGAGATCATGTCTGACTGGGAGAGGTTTCCTTGGCAGCAGAGGACGCTAGGTTTGGG ATG AAA      2
                                                                                               6
E  A  G  Q  M  Q  N  L  E  S  A  R  A  G  R  S  V  S  T  Q      22
GAA GCT GGG CAG ATG CAA AAT CTG GAG AGC GCG AGG GCC GGG CGG TCA GTC AGC ACC CAG      66
T  G  S  M  T  G  Q  I  P  R  L  S  K  V  N  L  F  T  L  L      42
ACT GGC AGC ATG ACC GGT CAG ATA CCA AGG CTT TCT AAA GTC AAC CTT TTC ACT CTG CTC      126
S  L  W  M  E  L  F  P  A  E  A  Q  R  Q  K  S  Q  K  N  E      62
AGC CTC TGG ATG GAG CTC TTT CCA GCA GAA GCC CAG CGG CAA AAA TCT CAG AAA AAT GAA      186
E  G  K  H  G  P  L  G  D  N  E  E  R  T  R  V  S  T  D  K      82
GAG GGA AAG CAT GGA CCC TTA GGA GAT AAT GAA GAG AGG ACC AGA GTA TCT ACT GAC AAA      246
R  Q  V  K  R  T  G  L  V  V  V  K  N  M  K  I  V  G  L  H      102
AGA CAG GTA AAG AGA ACT GGT CTT GTG GTG GTG AAA AAC ATG AAA ATT GTT GGT CTC CAC      306
C  S  S  E  D  L  H  A  G  Q  I  A  L  I  K  H  G  S  R  L      122
TGT TCT AGT GAA GAT TTA CAT GCC GGG CAG ATT GCT CTT ATT AAA CAT GGG TCA AGG CTG      366
K  N  C  D  L  Y  F  S  R  K  P  C  S  A  C  L  K  M  I  V      142
AAA AAC TGT GAT CTT TAT TTT TCC AGA AAA CCA TGT TCT GCT TGT TTG AAA ATG ATT GTA      426
N  A  G  V  N  R  I  S  Y  W  P  A  D  P  E  I  S  L  L  T      162
AAT GCT GGA GTT AAC CGA ATT TCA TAC TGG CCT GCT GAT CCA GAA ATA AGT TTG CTT ACG      486
E  A  S  S  S  E  D  A  K  L  D  A  K  A  V  E  R  L  K  S      182
GAG GCT TCT AGT TCT GAA GAT GCA AAG TTA GAT GCC AAA GCA GTG GAA AGA TTG AAG TCA      546
N  S  R  A  H  V  C  V  L  L  Q  P  L  V  C  Y  M  V  Q  F      202
AAC AGT CGG GCC CAT GTG TGT GTC TTA CTT CAA CCT TTG GTG TGT TAT ATG GTG CAG TTT      606
V  E  E  T  S  Y  K  C  D  F  I  Q  K  I  T  K  T  L  P  D      222
GTA GAG GAG ACC TCT TAC AAA TGT GAC TTT ATT CAA AAA ATT ACA AAA ACA TTG CCG GAT      666
A  N  T  D  F  Y  Y  E  C  K  Q  E  R  I  K  E  Y  E  M  L      242
GCT AAC ACT GAC TTT TAT TAT GAA TGT AAA CAA GAA AGA ATA AAA GAA TAT GAA ATG TTA      726
F  L  V  S  N  E  E  M  H  K  Q  I  L  M  T  I  G  L  E  N      262
TTT TTG GTT TCA AAT GAA GAA ATG CAT AAG CAA ATA CTG ATG ACT ATA GGT TTG GAG AAC      786
L  C  E  N  P  Y  F  S  N  L  R  Q  N  M  K  D  L  I  L  L      282
CTG TGT GAA AAT CCA TAC TTT AGC AAT CTA AGG CAA AAC ATG AAA GAC CTT ATC CTA CTT      846
L  A  T  V  A  S  S  V  P  N  F  K  H  F  G  F  Y  R  S  N      302
TTG GCC ACA GTA GCT TCC AGT GTG CCG AAC TTT AAA CAC TTC GGA TTT TAC CGT AGC AAT      906
P  E  Q  I  N  E  I  H  N  Q  S  L  P  Q  E  I  A  R  H  C      322
CCA GAA CAG ATT AAT GAA ATT CAC AAT CAA AGT TTG CCA CAG GAA ATT GCA AGG CAC TGC      966
M  V  Q  A  R  L  L  A  Y  R  T  G  E  L  H  R  S  *      340
ATG GTT CAG GCC AGG TTA TTG GCA TAT CGA ACT GGT GAG TTA CAT AGA TCG TAA      1020

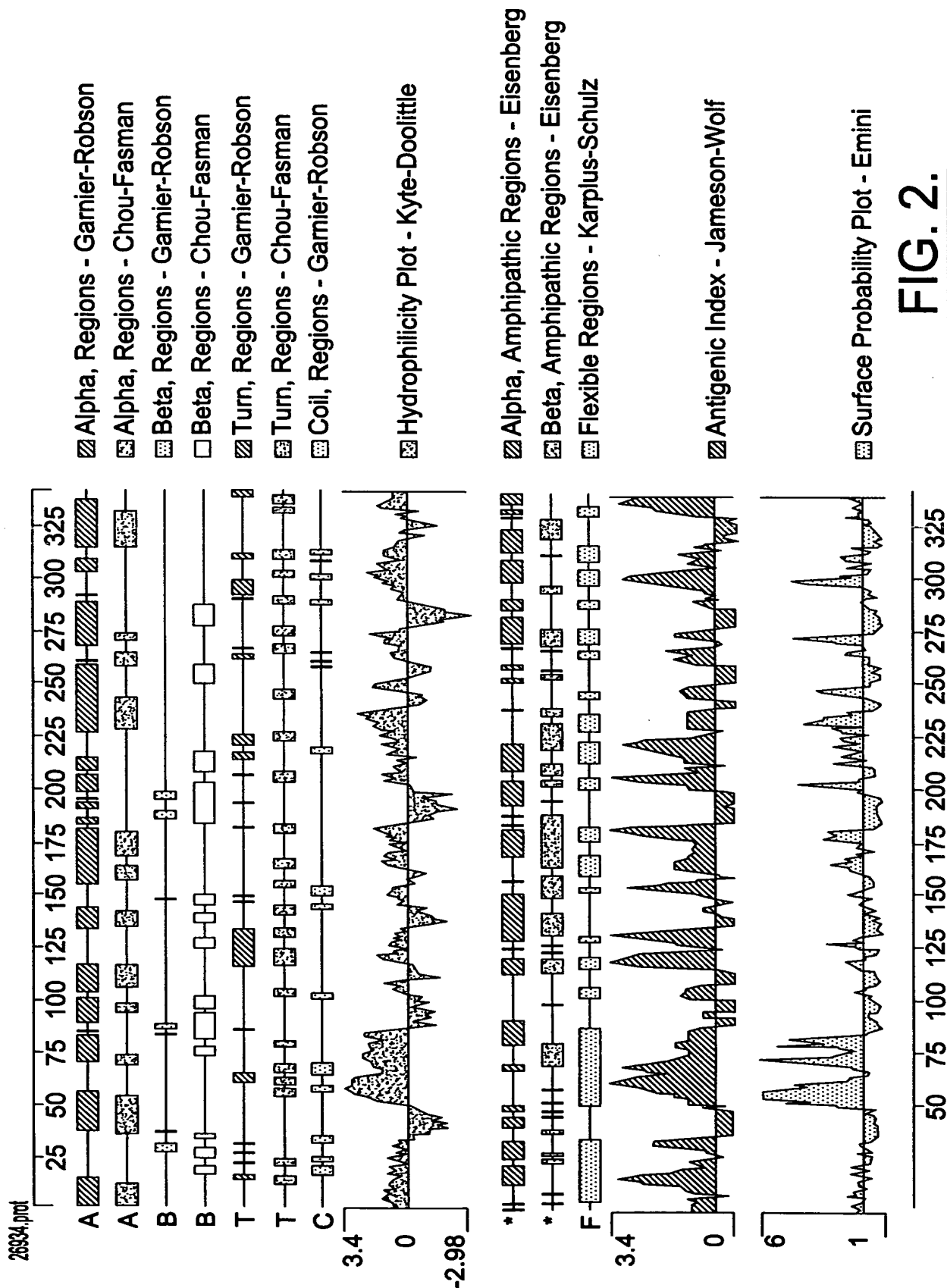
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ATTGGGGCTGATTGGTTGGGTTGATTTGTCTCTGAAGTGTTCTGCTCATTTATGGTAGAGTTCATTTACTCATAGTTA

FIG. 1A.

CTTAAGTTTGTGCTTCATACAATATAGAGAAGTTAGTGAGACCCTTGAGTAGACAACCTTTTCTCCCAGCAGTTTTGG
GATTCCTTGAGCCTTATATTCAGTACCACATTTCTACATCAGGCCCTCATTAACTAGGCCCTTCTTTCTGCTTCTTG
CTTTTATGATTTCACTGKTCCTTGAGCCCTCCACTAAAGGTAGGACAAGAAGAGAAAGGAGAGGCCCACTGCAGTGGTT
CATGCCTGTAATTGCAACACTTTAGAAGGCTGADACAGGAGGATCGCTTGAGCTCAGGAGTTCAAGACCAGCGTGGGCA
ACATAGCAAGACCTCGACTCTA

FIG. 1B.



Protein Family / Domain Matches, HMMer version 2

Searching for complete domains in PFAM
 hmmpfam - search a single seq against HMM database
 HMMER 2.1.1 (Dec 1998)
 Copyright (C) 1992-1998 Washington University School of Medicine
 HMMER is freely distributed under the GNU General Public License (GPL).

HMM file: /prod/ddm/seqanal/PFAM/pfam4.4/Pfam
 Sequence file: /tmp/orfanal.14420.aa

Query: 26934

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
dCMP_cyt_deam	Cytidine and deoxycytidylate deaminase	26.8	0.00052	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
dCMP_cyt_deam	1/1	80	149	1	100	26.8	0.00052

Alignments of top-scoring domains:

dCMP_cyt_deam: domain 1 of 1, from 80 to 149: score 26.8, E = 0.00052

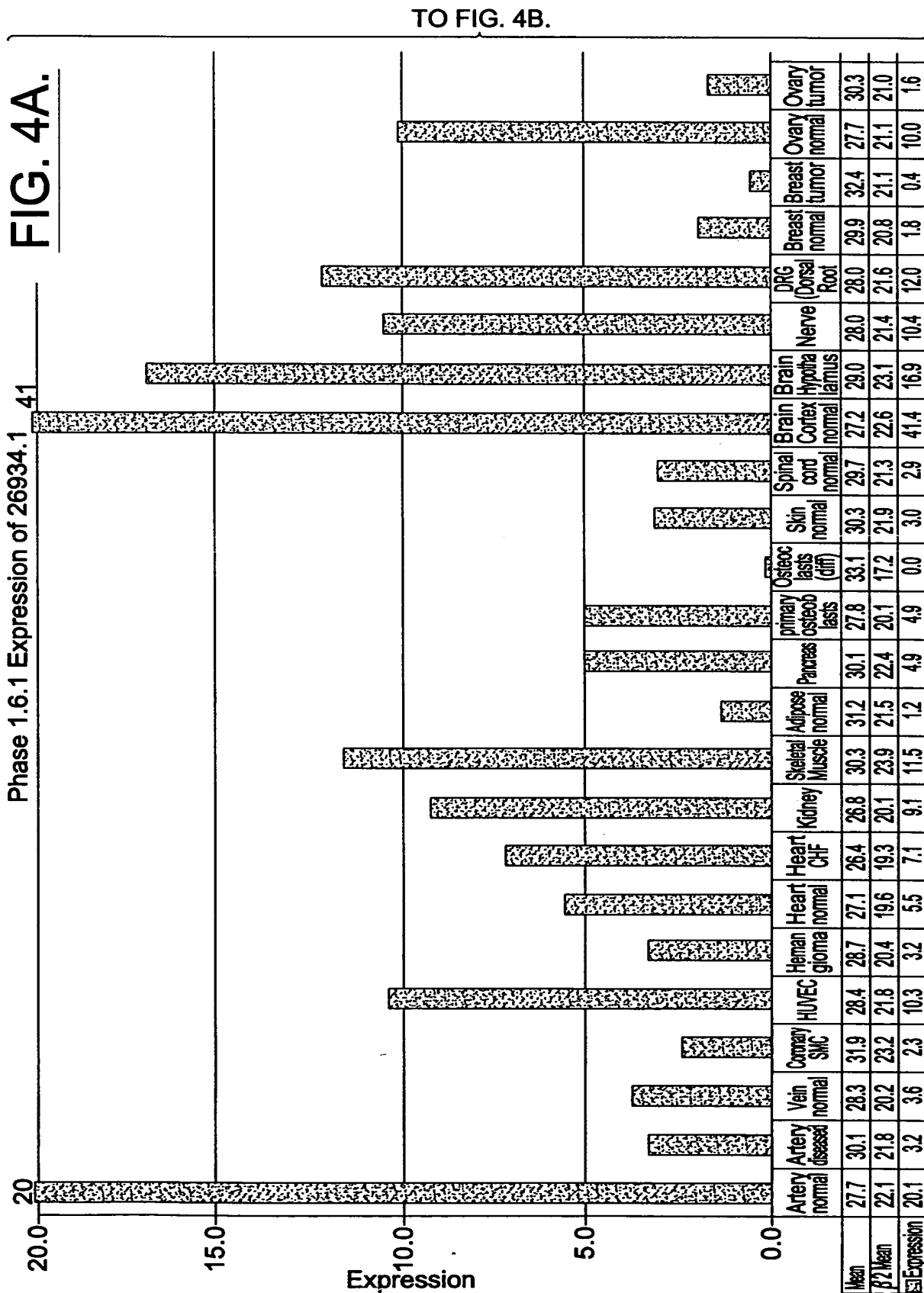
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      *->tpysgfpvGavivkdnGrifgvnseganyveGeqkkdptaHAEvnAI
            t++ ++++ +v tn      ++ ++++e      +HA + A+
26934    80  TDKRQVKRTGLVVVKN---MKIVGLHCSSE-----DLHAGQIAL 115

            rkAvseryrdFkir1gger1egat1YvT1ePCgHyGRTpmCaqa1iesgi
            +K      +      r1++++1Y + PC      C ++i+++g+
26934    116 IK-H--G-----SRLKNCPLYFSRKPC-----SACLKMIYNAGV 146

            kkV<-*
            ++
26934    147 NRI      149
  
```

FIG. 3.



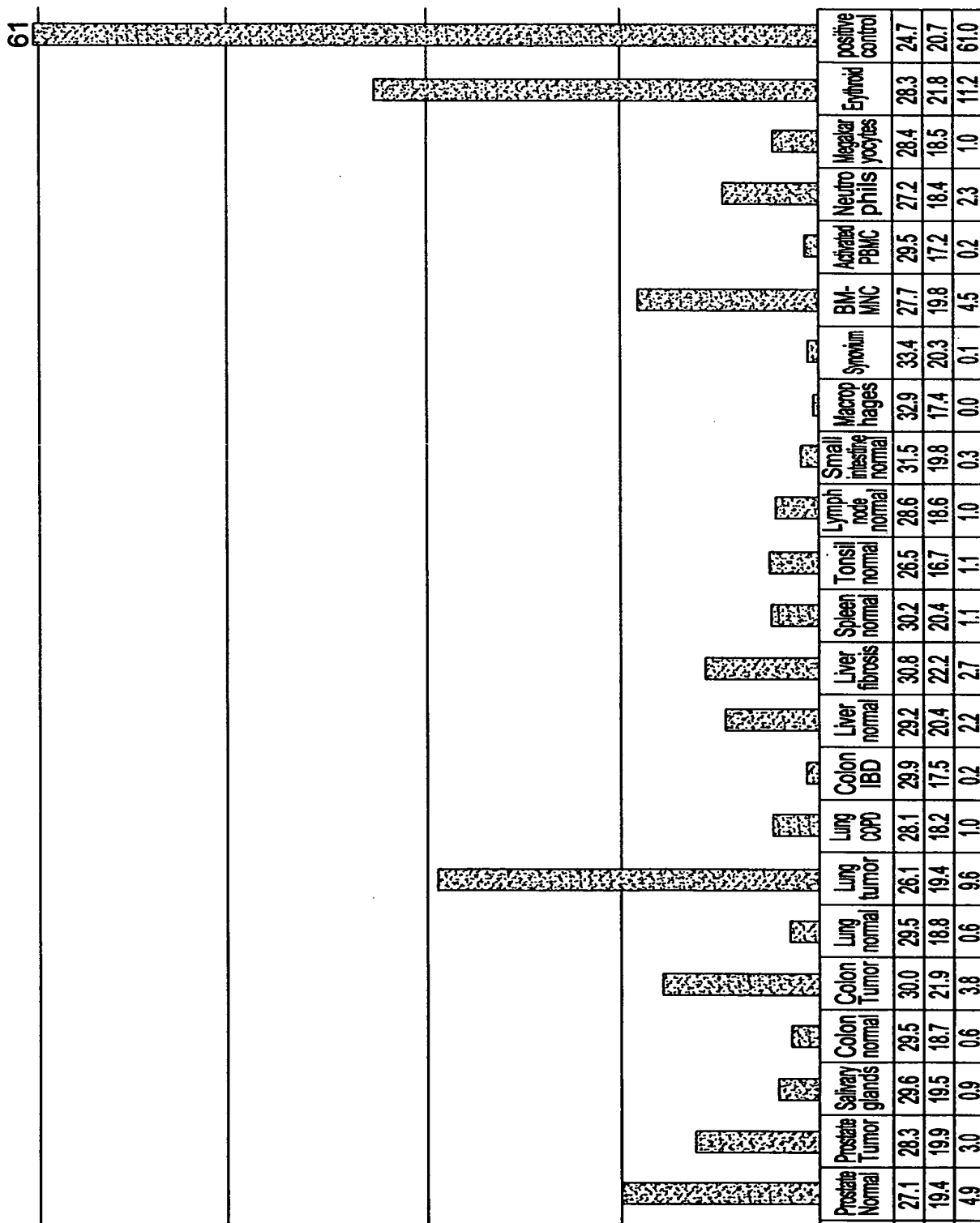


FIG. 4B.

FROM FIG. 4A.

35

26934.1 Expression in Oncology Phase II Plate

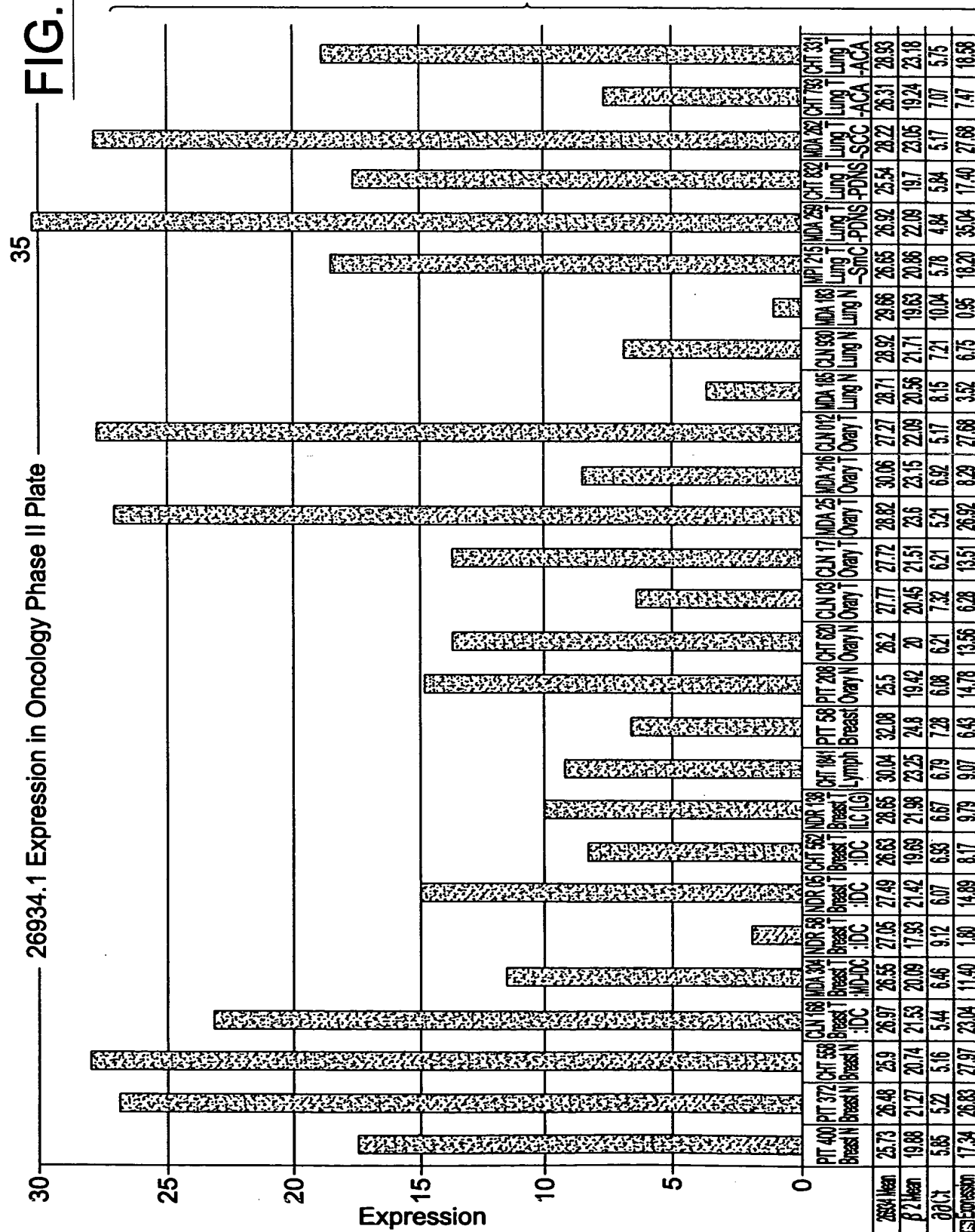
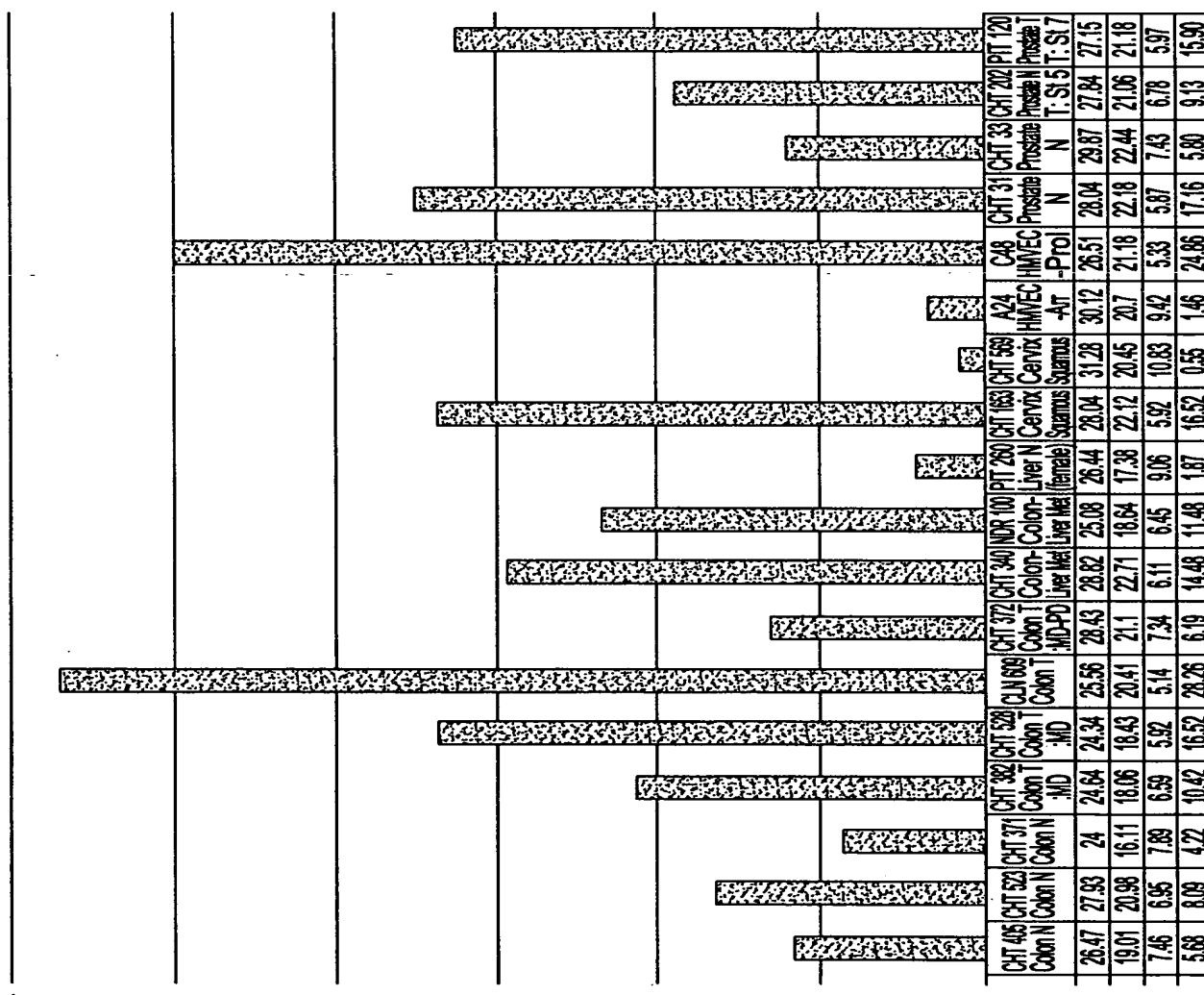


FIG. 5B.



FROM FIG. 5A.

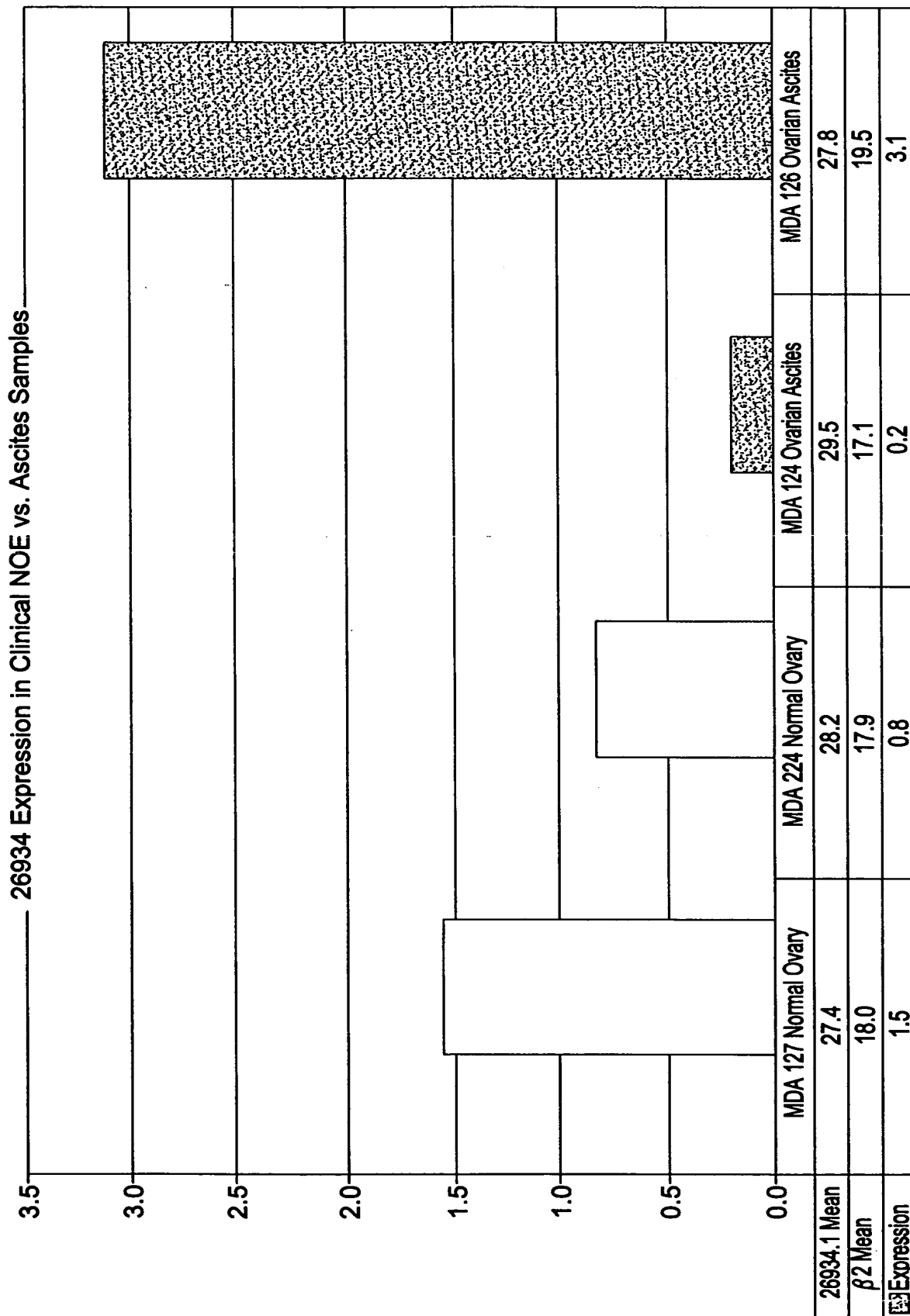


FIG. 6.

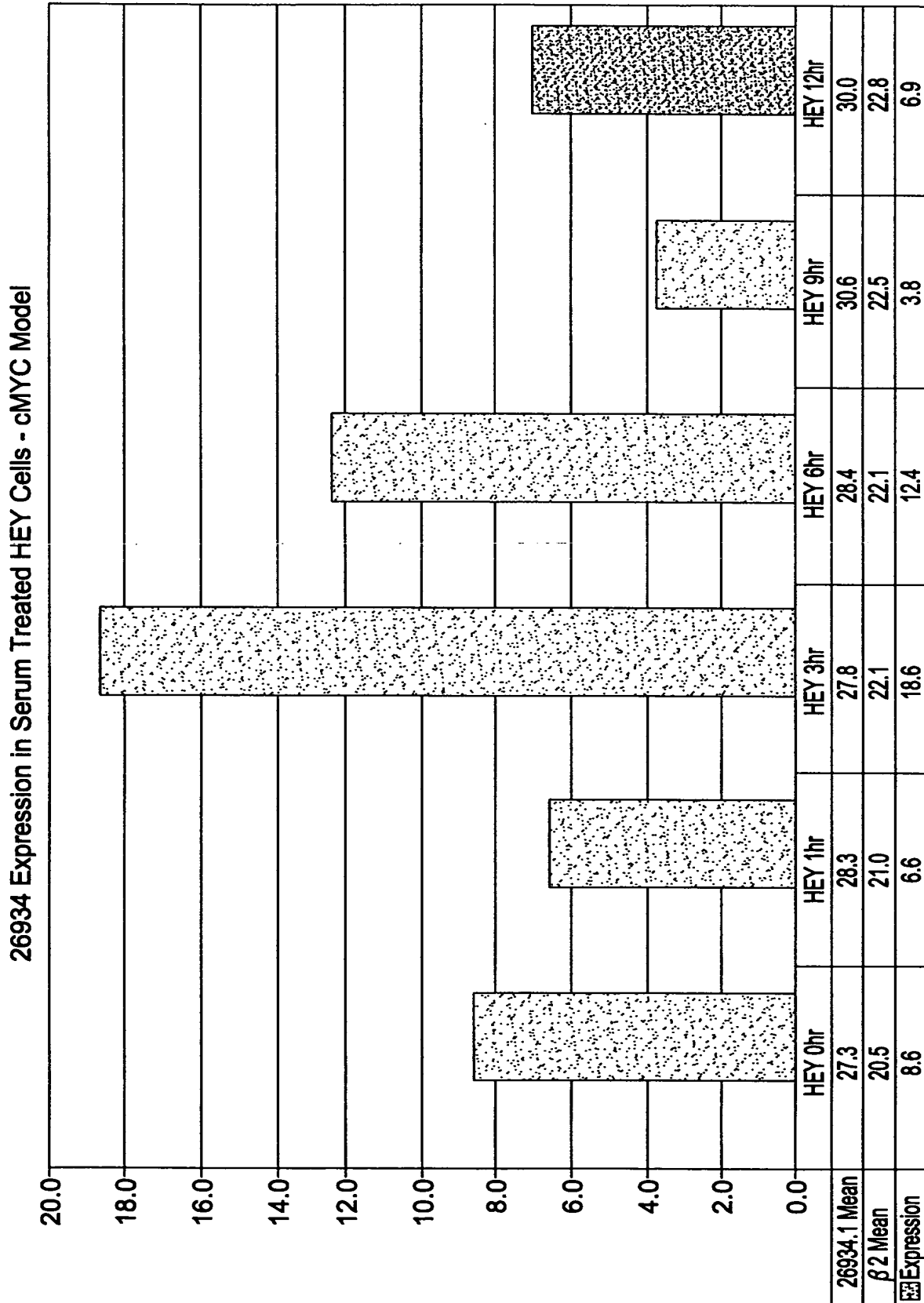


FIG. 7.

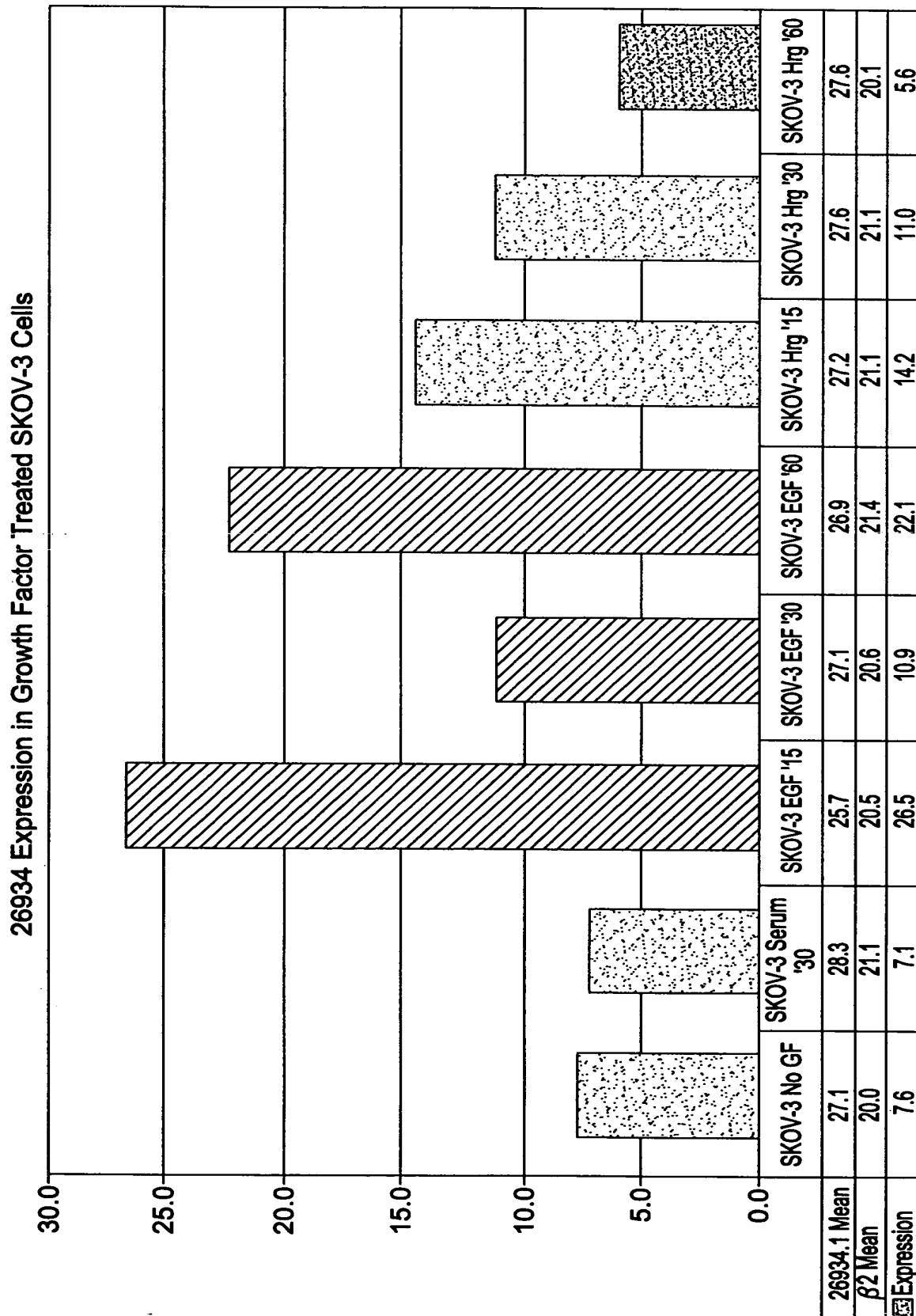


FIG. 8.

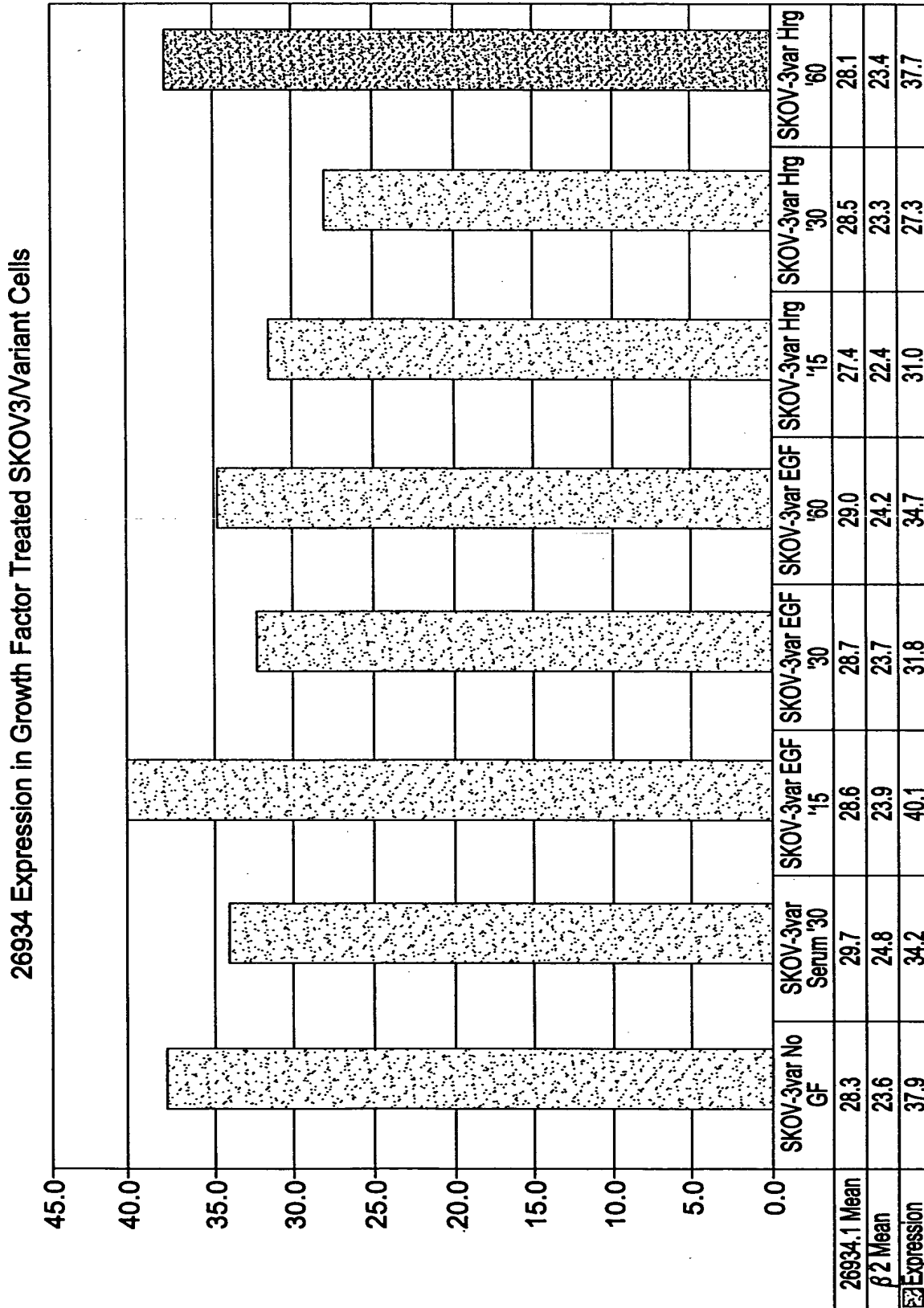


FIG. 9.

FIG. 10A.

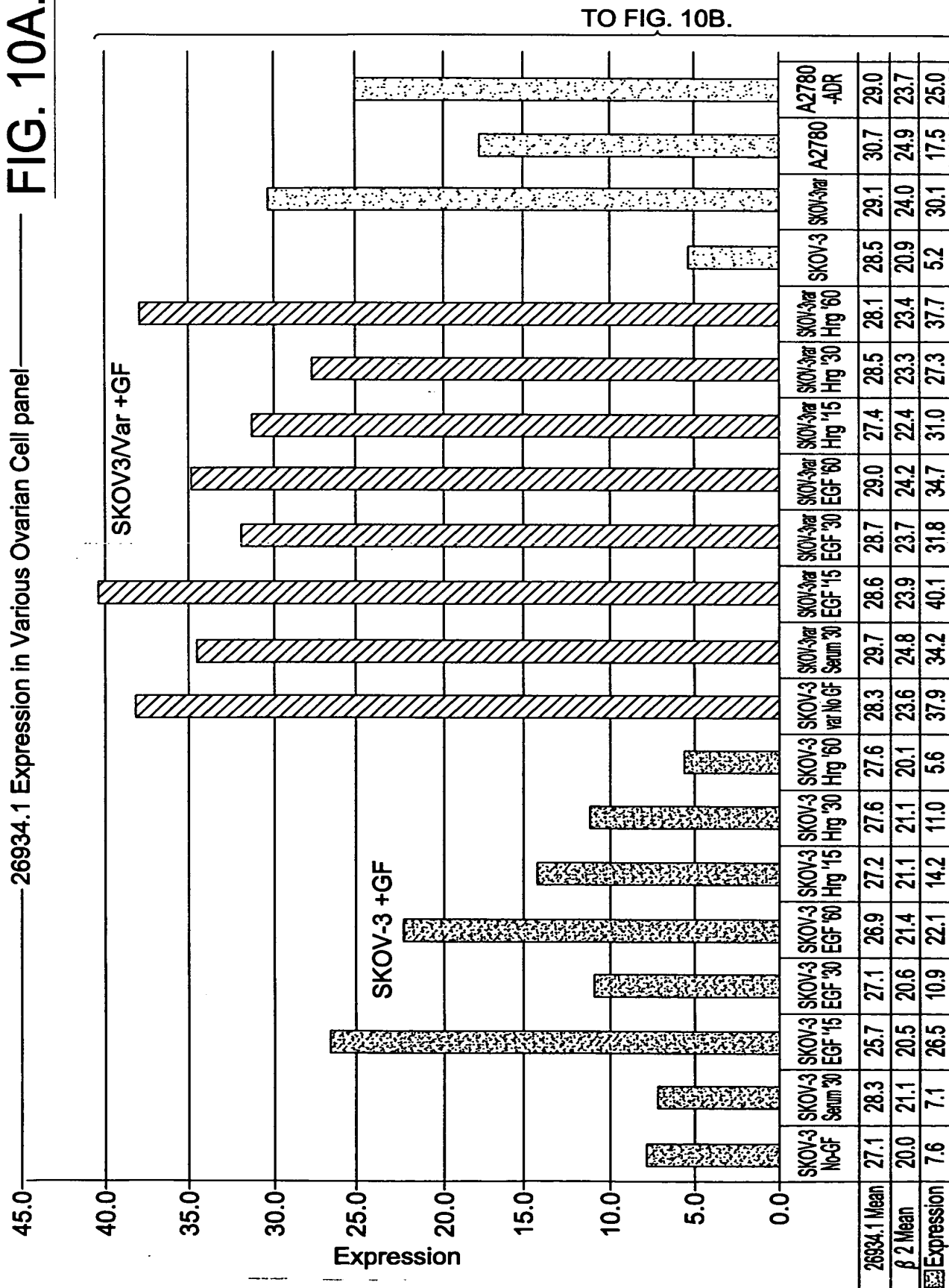


FIG. 10B.

